

RAW SEQUENCE LISTING

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Application Serial Number: 10/540,846
Source: IFWP
Date Processed by STIC: 06/21/2006

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IFWP

RAW SEQUENCE LISTING

DATE: 06/21/2006

PATENT APPLICATION: US/10/540,846

TIME: 10:16:53

Input Set : E:\ARS-111 seq-listing.replace.txt

Output Set: N:\CRF4\06212006\J540846.raw

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3 <110> APPLICANT: Bienkowska, Jadwiga
4   Mcallister, Gregg
6 <120> TITLE OF INVENTION: NOVEL FIBULIN-LIKE POLYPEPTIDES
8 <130> FILE REFERENCE: ARS-111
10 <140> CURRENT APPLICATION NUMBER: US 10/540,846
11 <141> CURRENT FILING DATE: 2005-06-27
13 <150> PRIOR APPLICATION NUMBER: US 60/436,786
14 <151> PRIOR FILING DATE: 2002-12-27
16 <160> NUMBER OF SEQ ID NOS: 4
18 <170> SOFTWARE: PatentIn version 3.1
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21 <211> LENGTH: 2661
22 <212> TYPE: DNA
23 <213> ORGANISM: homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: misc_feature
27 <222> LOCATION: (50)..(2582)
28 <223> OTHER INFORMATION: SCS0007 polynucleotide coding sequence
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35 caccgggagg aagccgccc ggcacttcgc ggccgagaga cgccgactgg gccccacgt      180
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53 ctgtcgaact ggcttcacc ttcatggcaa ccggcactcc tgtgtagatg taaacgagtg      720
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63 gtgtcgtgca tgtttcgtga gtgtcctttt ggcccgtgtg agacccccca taaagacgga     1020
65 ttgctgtact tgtgttcag tgagatgcta tttccacggc cgggtggtacg cagacggggc     1080
67 tgtgttcagt gggggtggtg acgagtgtac cacctgtgtt tgccagaatg gggaggtgga     1140
69 gtgtccttc atgccctgcc ctgagctggc ctgccccga gaagagtggc ggctgggccc     1200
71 tgggcagtgt tgcttcacct gccaggagcc cacaccctcg acaggctgct ctcttgacga     1260
73 caacgggggt gagttccga ttggacagat ctggtcgcct ggtgaccct gtgagttatg     1320
75 catctgccag gcagatggct cggtagctg caagaggaca gactgtgtgg actcctgccc     1380
77 tcaccgcgac cggatccctg gacagtgtg cccagactgt tcagcagctg gtgctcagcg     1440

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85 cgtgtgccga gactgcaact acgaggaag gaaggtggcg aatggccagg tgttcacctt 1680
87 ggatgatgaa cctgcaccc ggtgcacgtg ccagctggga gaggtgagct gtgagaaggt 1740
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91 tccagattcc ctgtctctc tggaagaaaa gcaggggctc tccctcacg gaaatgtggc 1860
93 attcagcaaa gctggtcgga gcctgcatgg agacactgag gcccctgtca actgtagctc 1920
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115 gtggttaagt agcatccacc tttaccccac tgctggggag aaaagctggc accaaattgt 2580
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122 <210> SEQ ID NO: 2

123 <211> LENGTH: 818

124 <212> TYPE: PRT

125 <213> ORGANISM: homo sapiens

127 <400> SEQUENCE: 2

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132 Pro Gly Ala Pro Ala Arg Gly Tyr Thr Gly Arg Lys Pro Pro Gly His
133 20 25 30
135 Phe Ala Ala Glu Arg Arg Arg Leu Gly Pro His Val Cys Leu Ser Gly
136 35 40 45
138 Phe Gly Ser Gly Cys Cys Pro Gly Trp Ala Pro Ser Met Gly Gly Gly
139 50 55 60
141 His Cys Thr Leu Pro Leu Cys Ser Phe Gly Cys Gly Ser Gly Ile Cys
142 65 70 75 80
144 Ile Ala Pro Asn Val Cys Ser Cys Gln Asp Gly Glu Gln Gly Ala Thr
145 85 90 95
147 Cys Pro Glu Thr His Gly Pro Cys Gly Glu Tyr Gly Cys Asp Leu Thr
148 100 105 110
150 Cys Asn His Gly Gly Cys Gln Glu Val Ala Arg Val Cys Pro Val Gly
151 115 120 125
153 Phe Ser Met Thr Glu Thr Ala Val Gly Ile Arg Cys Thr Asp Ile Asp
154 130 135 140
156 Glu Cys Val Thr Ser Ser Cys Glu Gly His Cys Val Asn Thr Glu Gly
157 145 150 155 160
159 Gly Phe Val Cys Glu Cys Gly Pro Gly Met Gln Leu Ser Ala Asp Arg
160 165 170 175
162 His Ser Cys Gln Asp Thr Asp Glu Cys Leu Gly Thr Pro Cys Gln Gln

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163				180				185					190				
165	Arg	Cys	Lys	Asn	Ser	Ile	Gly	Ser	Tyr	Lys	Cys	Ser	Cys	Arg	Thr	Gly	
166			195					200					205				
168	Phe	His	Leu	His	Gly	Asn	Arg	His	Ser	Cys	Val	Asp	Val	Asn	Glu	Cys	
169		210					215					220					
171	Arg	Arg	Pro	Leu	Glu	Arg	Arg	Val	Cys	His	His	Ser	Cys	His	Asn	Thr	
172	225					230					235					240	
174	Val	Gly	Ser	Phe	Leu	Cys	Thr	Cys	Arg	Pro	Gly	Phe	Arg	Leu	Arg	Ala	
175				245						250						255	
177	Asp	Arg	Val	Ser	Cys	Glu	Gly	Ala	Leu	Ser	Pro	Pro	Asp	Trp	Gln	Gln	
178				260					265					270			
180	Gly	Pro	Leu	Pro	Ala	Gly	Thr	Trp	Glu	Pro	Cys	Met	Asn	Gln	Gly	Val	
181			275					280					285				
183	Ala	Gly	Gln	Ser	Leu	Gly	Val	Pro	Ser	Ala	Gly	Ala	Arg	Leu	Glu	Thr	
184		290					295					300					
186	Cys	Arg	Ala	Cys	Phe	Val	Ser	Val	Leu	Leu	Ala	Arg	Val	Arg	Pro	Pro	
187	305					310					315					320	
189	Ile	Lys	Thr	Asp	Cys	Cys	Thr	Cys	Val	Pro	Val	Arg	Cys	Tyr	Phe	His	
190				325						330					335		
192	Gly	Arg	Trp	Tyr	Ala	Asp	Gly	Ala	Val	Phe	Ser	Gly	Gly	Gly	Asp	Glu	
193				340					345					350			
195	Cys	Thr	Thr	Cys	Val	Cys	Gln	Asn	Gly	Glu	Val	Glu	Cys	Ser	Phe	Met	
196			355					360					365				
198	Pro	Cys	Pro	Glu	Leu	Ala	Cys	Pro	Arg	Glu	Glu	Trp	Arg	Leu	Gly	Pro	
199		370					375					380					
201	Gly	Gln	Cys	Cys	Phe	Thr	Cys	Gln	Glu	Pro	Thr	Pro	Ser	Thr	Gly	Cys	
202	385					390					395					400	
204	Ser	Leu	Asp	Asp	Asn	Gly	Val	Glu	Phe	Pro	Ile	Gly	Gln	Ile	Trp	Ser	
205				405						410					415		
207	Pro	Gly	Asp	Pro	Cys	Glu	Leu	Cys	Ile	Cys	Gln	Ala	Asp	Gly	Ser	Val	
208				420					425					430			
210	Ser	Cys	Lys	Arg	Thr	Asp	Cys	Val	Asp	Ser	Cys	Pro	His	Pro	Ile	Arg	
211			435					440					445				
213	Ile	Pro	Gly	Gln	Cys	Cys	Pro	Asp	Cys	Ser	Ala	Ala	Gly	Ala	Gln	Arg	
214		450					455					460					
216	Met	Leu	Ser	Leu	Ala	Gly	Cys	Thr	Tyr	Thr	Gly	Arg	Ile	Phe	Tyr	Asn	
217	465					470					475					480	
219	Asn	Glu	Thr	Phe	Pro	Ser	Val	Leu	Asp	Pro	Cys	Leu	Ser	Cys	Ile	Cys	
220				485						490					495		
222	Leu	Leu	Gly	Ser	Val	Ala	Cys	Ser	Pro	Val	Asp	Cys	Pro	Ile	Thr	Cys	
223				500					505					510			
225	Thr	Tyr	Pro	Phe	His	Pro	Asp	Gly	Glu	Cys	Cys	Pro	Val	Cys	Arg	Asp	
226			515					520					525				
228	Cys	Asn	Tyr	Glu	Gly	Arg	Lys	Val	Ala	Asn	Gly	Gln	Val	Phe	Thr	Leu	
229		530					535					540					
231	Asp	Asp	Glu	Pro	Cys	Thr	Arg	Cys	Thr	Cys	Gln	Leu	Gly	Glu	Val	Ser	
232	545					550					555					560	
234	Cys	Glu	Lys	Val	Pro	Cys	Gln	Arg	Ala	Cys	Ala	Asp	Pro	Ala	Leu	Leu	
235				565						570					575		

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237 Pro Gly Asp Cys Cys Ser Ser Cys Pro Asp Ser Leu Ser Pro Leu Glu
238          580          585          590
240 Glu Lys Gln Gly Leu Ser Pro His Gly Asn Val Ala Phe Ser Lys Ala
241          595          600          605
243 Gly Arg Ser Leu His Gly Asp Thr Glu Ala Pro Val Asn Cys Ser Ser
244          610          615          620
246 Cys Pro Gly Pro Pro Thr Ala Ser Pro Ser Arg Pro Val Leu His Leu
247 625          630          635          640
249 Leu Gln Leu Leu Leu Arg Thr Asn Leu Met Lys Thr Gln Thr Leu Pro
250          645          650          655
252 Thr Ser Pro Ala Gly Ala His Gly Pro His Ser Leu Ala Leu Gly Leu
253          660          665          670
255 Thr Ala Thr Phe Pro Gly Glu Pro Gly Ala Ser Pro Arg Leu Ser Pro
256          675          680          685
258 Gly Pro Ser Thr Pro Pro Gly Ala Pro Thr Leu Pro Leu Ala Ser Pro
259          690          695          700
261 Gly Ala Pro Gln Pro Pro Pro Val Thr Pro Glu Arg Ser Phe Ser Ala
262 705          710          715          720
264 Ser Gly Ala Gln Ile Val Ser Arg Trp Pro Pro Leu Pro Gly Thr Leu
265          725          730          735
267 Leu Thr Glu Ala Ser Ala Leu Ser Met Met Asp Pro Ser Pro Ser Lys
268          740          745          750
270 Thr Pro Ile Thr Leu Leu Gly Pro Arg Val Leu Ser Pro Thr Thr Ser
271          755          760          765
273 Arg Leu Ser Thr Ala Leu Ala Ala Thr Thr His Pro Gly Pro Gln Gln
274          770          775          780
276 Pro Pro Val Gly Ala Ser Arg Gly Glu Glu Ser Thr Met Leu Ser Arg
277 785          790          795          800
279 Phe Pro His Ala Ala Leu Leu Ile His Arg Leu Pro Val Gly Arg Trp
280          805          810          815
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286 <211> LENGTH: 2397
287 <212> TYPE: DNA
288 <213> ORGANISM: homo sapiens
290 <400> SEQUENCE: 3
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299 catggaccat gtggggagta cggctgtgac cttacctgca accatggagg ctgtcaggag      300
301 gtggcccag tgtgccccgt gggcttctcg atgacggaga cagctgttgg catcagggtg      360
303 acagacattg acgaatgtgt aacctcctcc tgcgagggcc actgtgtgaa cacagaaggt      420
305 gggtttgtgt gcgagtgtgg gccgggcatg cagctgtctg ccgaccgcca cagctgcca      480
307 gacactgacg aatgcctagg gactccctgt cagcagagat gtaaaaacag cattggcagc      540
309 tacaagtgtt cctgtcgaac tggcttcac cttcatggca accggcactc ctgtgtagat      600
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321 ataaagacgg attgctgtac ttgtgttcca gtgagatgct atttccacgg ccggtgggtac      960
323 gcagacgggg ctgtgttcag tgggggtggg gacgagtgtg ccacctgtgt ttgccagaat     1020
325 ggggaggtgg agtgctcctt catgccctgc cctgagctgg cctgcccccg agaagagtgg     1080
327 cggctggggc ctgggcagtg ttgcttcacc tgccaggagc ccacaccctc gacaggctgc     1140
329 tctcttgacg acaacggggg tgagtttccg attggacaga tctgggtcgcc tggtgacccc     1200
331 tgtgagttat gcatctgcca ggcagatggc tcggtgagct gcaagaggac agactgtgtg     1260
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341 gagtgtgcc ccgtgtgccg agactgcaac tacgagggaa ggaaggtggc gaatggccag     1560
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367 ggccccccagc agccccagc gggggcttct cggggggaag agtccaccat gttgtctcgg     2340
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372 <210> SEQ ID NO: 4

373 <211> LENGTH: 798

374 <212> TYPE: PRT

375 <213> ORGANISM: homo sapiens

377 <400> SEQUENCE: 4

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383 20 25 30
385 Cys Cys Pro Gly Trp Ala Pro Ser Met Gly Gly Gly His Cys Thr Leu
386 35 40 45
388 Pro Leu Cys Ser Phe Gly Cys Gly Ser Gly Ile Cys Ile Ala Pro Asn
389 50 55 60
391 Val Cys Ser Cys Gln Asp Gly Glu Gln Gly Ala Thr Cys Pro Glu Thr
392 65 70 75 80
394 His Gly Pro Cys Gly Glu Tyr Gly Cys Asp Leu Thr Cys Asn His Gly
395 85 90 95
397 Gly Cys Gln Glu Val Ala Arg Val Cys Pro Val Gly Phe Ser Met Thr
398 100 105 110
400 Glu Thr Ala Val Gly Ile Arg Cys Thr Asp Ile Asp Glu Cys Val Thr
401 115 120 125
403 Ser Ser Cys Glu Gly His Cys Val Asn Thr Glu Gly Gly Phe Val Cys

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